

# Untitled-12 Formatted Alignment

HTLV-III: HIV-I  
Env Alignment

HTLV-II Env	M-----GNVF--FLF-----LFS-----	11
HTLV-I Env	-----GKFLATLIL-----FFQ-----	13
HIV SF2 Env	MTARGTRKNYQRLWRWGIML LGMLMICSAA ENLWVTVYVG VPVWKEATTT	50
Consensus	M-----G..L...LI-----F.-----	50
HTLV-II Env	-LT--HFPLAQ--QS-----R-----TLTIC--IS--SY-----	32
HTLV-I Env	-FC--PLIFGDYSP-----C-----TLTIC--VS--SY-----	36
HIV SF2 Env	LFCASDARAYATEVHNWVATHAQVPTDPNPQEVVLGNVTE NFDMWKNNMV	100
Consensus	-FC-----A....S-----C-----TLTIC--S--SY-----	100
HTLV-II Env	-----SS--SPGSP--TQFV-----	45
HTLV-I Env	-----SS--KPCNP--AQFV-----	49
HIV SF2 Env	EQMQEDIISLWDGSLKPCVKLTFLQVTLDC TDVNTTSSSL RNATNTTSSS	150
Consensus	-----SS--KPC.P--QFV-----S-----	150
HTLV-II Env	-----NEELNSLT--TDC--RL--H-----	60
HTLV-I Env	-----TEELLALS--ADC--AL--Q-----	64
HIV SF2 Env	MEIMEKGELKNCSFNITTSIRDKMQEQYALFYKLDVLPIDKNETKFRLLH	200
Consensus	-----LLELL.L..DC--RL--H-----	200
HTLV-II Env	-----PFCFNL-----I--TY--SGF-----HKTYS-----	77
HTLV-I Env	-----PFCFNL-----V--SY--SSY-----HATYS-----	81
HIV SF2 Env	CNTSTITQACPKISFEPIPMHYCTPAGFAILKCNDKKFNGTGPCTNVSTV	250
Consensus	-----PFCFNL-----M--SGF-----HKTYS-----	250
HTLV-II Env	-----TME-----	81
HTLV-I Env	-----TME-----	85
HIV SF2 Env	QCTHGIKPVVSTQILLNGSLAEEVEVIIRSSNFINNAKIII VQLNKSVEIN	300
Consensus	-----TME-----S-----	300
HTLV-II Env	-----TME-----	86
HTLV-I Env	-----TME-----	90
HIV SF2 Env	CTRENNNTRNRISIGPGRAFHTTKQIIGDIRQAHCNLSRA TWEKITLEQIA	350
Consensus	-----TME-----M.K-----	350
HTLV-II Env	-----KPNR--GLGYSSFSYN--DE-----GS--LQCP--Y-----	110
HTLV-I Env	-----KPNR--GGGYSSAAYS--DE-----GS--LKCP--Y-----	114
HIV SF2 Env	TKLRFQFFNK TIAFDRSSGGDEEIVMHSFN GGEFFYCN TSQLFNSTWND	400
Consensus	-----KPNR--G.GYSS.SY--DE-----GS--L.QP--Y-----	400
HTLV-II Env	-----TCC-----GAK--TS--AYTGPFSS--	126
HTLV-I Env	-----TCC-----SA--TC--PYTGAVSS--	130
HIV SF2 Env	TTRANSTEVTTLEPRIKQIVMMDQEVGKAMYAPPISGQIRCSSKITGLL	450
Consensus	-----TCC-----G.A--T--M.DGPVSS--	450

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HTLV-II Env	-----P-----SA-----KF-----	131
HTLV-I Env	-----P-----YA-----KF-----	135
HIV SF2 Env	LTRDGGKNTT NGIEIFRPAG GDMRDNMRSE LMKYKVKVIE PLGVAPTAR	500
Consensus	-----P-----A-----KF-----	500
HTLV-II Env	-----HSD-----VN-----E-----	137
HTLV-I Env	-----QHD-----VN-----E-----	141
HIV SF2 Env	RRVVOREKRA VGMLGAMFLG FLGAAGSTMG ARSMTLTVQA RQLLSGIVQQ	550
Consensus	-----Q.D-----VN-----E-----	550
HTLV-II Env	-----IQ-----VSQVSLRL-----HFSK-----CGSS	156
HTLV-I Env	-----IQ-----VSRLNINL-----HFSK-----CGFP	160
HIV SF2 Env	QNNLLRAIEA QHLLQLTVW GIKQLQARVL AVERYLKDOO LLGIWGC SGK	600
Consensus	-----IQ-----VSQ.L..RL-----HFSK-----CG..	600
HTLV-II Env	M-----P-----E-----EYEA-----	163
HTLV-I Env	F-----P-----E-----EYEA-----	167
HIV SF2 Env	LICTTTVPWN ASWSNKSINE IWDNMTWMQW EREIDNYTHL IYTLIESQN	650
Consensus	.-----P-----E-----EYEA-----	650
HTLV-II Env	-----EC-----YDP---LAF ITSEPTQPPP TSPPLVHSD	191
HTLV-I Env	-----EC-----YDP---LAF LNTEPSQLPP TAPPLLPHSN	195
HIV SF2 Env	QQEKNEQELL ELDKWAGLWS WFSITNWLWY I-----	681
Consensus	-----EC-----YDP---LAF I..EP.Q.PP T.PPL...S.	700
HTLV-II Env	LEHVLTPSTS WTKILKFYQ LTLQSTNYSC MCVDRSSLS SWHLYLPNI	241
HTLV-I Env	LDHILEPSIP WSKLLTLAQ LTLQSTNYTC IVCIDRASLS TWHLYSPNV	245
HIV SF2 Env	-----RI---F-----II---GGIV GLRIVFAV-L	701
Consensus	L.H.L.PS.. W..KIL.FYQ LTLQSTNY.C IVCIDR.SLS .WHLYLPNI.	750
HTLV-II Env	GPQQTSSRT ILFPSALPA PP-SQFPFWT HCYCPRLQAI TTDNCNNSII	290
HTLV-I Env	SYP-SSSSTP LLYPSALPA PHLTLPFNWT HCFPQIQAI VSSPCHNSLI	294
HIV SF2 Env	SI---VNRVR QGYSELS-----FQTR-----	719
Consensus	SYP-..SS.. .LYPSALPA P-...PF.WT HCFQPR.QAI ....C.NS.I	800
HTLV-II Env	GPFFSLAPVP PPATRRRRAV PIAVWLVSAL AAGTGIAGGVTGSLSLASSK	340
HTLV-I Env	GPFFSLSPVP TLGSRSRRAV PVAVWLVSAL AMGAGVAGGVTGSMSLASGK	344
HIV SF2 Env	DE-----TOR-----CPDRPEGIEEE-----	735
Consensus	GPFFSL.PVP ....R.RRAV P.AVWLVSAL A.G.G.AGGVTGS.SLAS.K	850
HTLV-II Env	SLLLEVKKII SHLTQAIVKNHQNIIRVAQY AAQNRRGIDL LFWEGGGICK	390
HTLV-I Env	SLLHEVKKII SOLTQAIVKNHKNIIRKVAQY AAQNRRGIDL LFWEGGGICK	394
HIV SF2 Env	---GGFR---RDRSGRIVDGF-----LA---LWDE---LR	760
Consensus	SLL.EVKKII S.LTQAIVKNH.N.I.RVAQY AAQNRRGIDL LFWEGGGICK	900

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HTLV-II Env	AIQEQQCCFLN	ISNTHVSVLQ	ERPHEKRV	VI	TGWGLN	WELG	LSQAREALQ	440
HTLV-I Env	ALQEQCRCFPN	ITNSHVPHLQ	ERPHEENRVL		TGWGLN	WELG	LSQAREALQ	444
HIV SF2 Env	SL-CLFSYHR	LRDLILIVAR	IVELLGRGW		EVLKYWNL		EQYWSQLKN	808
Consensus	ALQEQC.F.N	I.N.HV.VLQ	ERPHE.EV.		TGWGLN.WELG		LSQAREALQ	950

HTLV-II Env	TGTHILALLL	LVILFGPCIL	ROIQALPQR		LQNRHNQYSL	INPEIM	486
HTLV-I Env	TGTHLVALLL	LVILAGPCIL	ROLRHLPSP		VRYPHYSL--	IKPEST	488
HIV SF2 Env	SVISLLNATA	IAVAEGTDRV	IEIVQRAYRA		FLNIPRRIRQ	GLERALT	855
Consensus	TGTHLLALLL	LVUL.GPCIL	ROI..LP.E		..N.H.....	I.PE..	997

HTLV-I/II Env  
ALIGNMENT

HTLV-II Env	MCNVF--FLLESLTHFPLA Q--QSGTLLTIGISSYHSSP GSEIDPVCITW	46
HTLV-I Env	MCKFLATLILFFQFCPLIFG DYSPGCLLTIGISSYHSP GNPAPQVCSA	50
Consensus	MC.....L..E.....S.....G.....T.....I.....G.....S.....Y.....H.....S.....P.....G.....S.....E.....I.....D.....P.....V.....C.....I.....T.....W.....	50
HTLV-II Env	NLDINSLITTDQRTHPPCPNLTITSGFFHTYSLYLEPFAWK KPNRCGLGY	96
HTLV-I Env	TLDLIALSADQALPPCPNLTYSSTHTYSLYLEPFAWK KPNRCGLGY	100
Consensus	..LDL..I..L..D..L..Q..T..P..P..C..P..N..L..T..I..T..S..G..F..H..T..Y..S..L..Y..L..E..P..F..A..W..K..K..P..N..R..C..G..L..G..Y..	100
HTLV-II Env	SESNDPCSLCPYLGGCAWTSATIGEVSSPWKPHSDVNFTQEVSOVEL	146
HTLV-I Env	SASNDPCSLKCPYLGGCAWTCPTIGEVSSPWKPHSDVNFTQEVSRINAI	150
Consensus	S..S..Y..D..P..C..S..L..C..P..Y..L..G..G..C..A..W..T..S..A..T..I..G..E..V..S..S..P..W..K..P..H..S..D..V..N..F..T..Q..E..V..S..O..V..E..L..	150
HTLV-II Env	RLHFSKCGSSMTLLVDAPGYDEWLTSEP TOHPPTEPPLVHISITTHVU	196
HTLV-I Env	NLHFSKCGFPFSLIVDAPGYDPIWFLNTEP SQHPPTEPPLLPHSNIDHIT	200
Consensus	..L..H..E..S..K..C..G..S..S..M..T..L..L..V..D..A..P..G..Y..D..E..W..L..T..S..E..P..T..O..H..P..P..T..E..P..P..L..V..H..I..S..I..T..T..H..V..U..	200
HTLV-II Env	TPSTSMITKTLKFTQLTLOSINYSQVQVD RSTLSWHVL YIPNISITPQQ	246
HTLV-I Env	EPSTPAKSKLLTTLQLTLOSINYSQVQVD RSTLSWHVL YIPNISITPQS	249
Consensus	..E..S..T..S..M..I..T..K..T..L..K..F..T..Q..L..T..L..O..S..I..N..Y..S..Q..V..Q..V..D..R..S..T..L..S..W..H..V..L..Y..I..P..N..I..S..I..T..P..Q..Q..	250
HTLV-II Env	TSSRTILFPSLALPAPP-SQPFNWTGQYQRIQATITDNCNNSITLPPPS	295
HTLV-I Env	SSSTPILMPSLALPAPHLTL PFNWTGFTDPIQATIVSSPCNNSITLPPPS	299
Consensus	..S..S..S..T..P..I..L..M..P..S..L..A..L..P..A..P..P..-..S..Q..P..F..N..W..T..G..Q..Y..Q..R..I..Q..A..T..I..T..D..N..C..N..N..S..I..T..L..P..P..P..S..	300
HTLV-II Env	LPPVEPPATRERRAVEIAVWLVSAIAAGIGVAGGVGSLSTASCKSDLE	345
HTLV-I Env	LPPVETLGSRERRAVEIAVWLVSAIAAGVAGGVGSMSTASCKSDLE	349
Consensus	..L..P..P..V..E..P..P..A..T..R..E..R..R..A..V..E..I..A..V..W..L..V..S..A..I..A..A..G..I..G..V..A..G..G..V..G..S..L..S..T..A..S..C..K..S..D..L..E..	350
HTLV-II Env	VEKDISHLITAVKNEKNILRLAQYAAQNRRCIDIDHEDWEOGGICVATQEO	395
HTLV-I Env	VEKDISHLITAVKNEKNILRLAQYAAQNRRCIDIDHEDWEOGGICVATQEO	399
Consensus	..V..E..K..D..I..S..H..L..I..T..A..V..K..N..E..K..N..I..L..R..L..A..Q..Y..A..A..Q..N..R..R..C..I..D..I..D..H..E..D..W..E..O..G..G..I..C..V..A..T..Q..E..O..	400
HTLV-II Env	GQFLNISNTHYSSTQERPPLEKRVITGAGL NNDIGLSQNA REATQICHTI	445
HTLV-I Env	QRFNMINSTYPLQERPPLEKRVITGAGL NNDIGLSQNA REATQICHTI	449
Consensus	..G..Q..F..L..N..I..S..N..T..H..Y..S..S..T..Q..E..R..P..P..L..E..K..R..V..I..T..G..A..G..L..N..N..D..I..G..L..S..Q..N..A..R..E..A..T..Q..I..C..H..T..I..	450
HTLV-II Env	LAAHGVVTFEPQIERQIQALEPRLQNRN QYSTINPEIM	486
HTLV-I Env	VAAHGVVTFEPQIERQLRHLPKRVRYPHYSL--INPESS	488
Consensus	..L..A..A..H..G..V..V..T..F..E..P..Q..I..E..R..Q..I..Q..A..L..E..P..R..L..Q..N..R..N..Q..Y..S..T..I..N..P..E..I..M..	491

## HILV-II R01 Alignment

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HTLV-II Pol	HTAPGLRSDG	SPQRAYLW	DOTREDDIT	PLESHETHSA	CKGELLATIC	600
HTLV-I Pol	NTAPGLRSDG	STSPRAYTLW	DKQILRSRFS	PLPPPH-KSA	ORAEILGLH	514
Consensus	HTAPGLRSDG	...RAYLW	...IT	PLE...	SA...EL...	600
HTLV-II Pol	GRPAKHP	ENLEEDSKYL	IKYHSLAIG	AFLEISAHQT	LOAPLPRLD	650
HTLV-I Pol	GLSSARSARC	ENLEEDSKYL	YHYRTEALG	IFGGRSSQAP	FOALLPRLLS	564
Consensus	GL...A...	ENLEEDSKYL	...ALG	IFGGRSS...	QA...LP...	650
HTLV-II Pol	GRVYLHHVR	SHTNLDPDPS	ITNEYMSLI	LAEVLVLPD	GLHGLTHCNC	700
HTLV-I Pol	RAVYLHHVR	SHTNLDPDPS	RLNALDAIL	ITFVLQLSPA	ELHSFTHCGC	614
Consensus	...K...VLAHHVR	SHTNLDPDPS	...N...D...	...E...E...	...LH...THC...	700
HTLV-II Pol	RAVSEGAIP	REAKSLVQIC	HICQTINSH	MPRCMIRRG	LIPNHIWGGD	750
HTLV-I Pol	TALTLOGAIT	TEASSILRSC	HAGRGNEOH	MPRGHIRRG	LIPNHIWGGD	664
Consensus	...AT...GA...	...RA...V...	...C...H...	...N...OH...	...MPRG...IRRG...	750
HTLV-II Pol	VTEKYYKYYK	YRLHWVDIE	SCAVSVCKK	KEKSCHEISA	MLQATSLGK	800
HTLV-I Pol	YTHFKYKNTL	YRLHWVDIE	SCAISCATKR	KEKSCSEATSS	MLQATIAHLGK	714
Consensus	...VTEKYYK...	Y...LHWVDIE...	SCA...S...	KEKSC...E...IS...	...LQAT...L...GK...	800
HTLV-II Pol	PLHINTDNGP	AYISCHQEF	CISYRIKHS	HDEYNPTSSG	LVERINGMLK	850
HTLV-I Pol	PSYINTDNGP	AYISCHQEF	CISLAIRHIT	HMPYNPTSSG	LVERINGMLK	764
Consensus	PL...INTDNGP	A...YISCH...	...IS...	...H...YNP...SSG...	...LVER...ING...MLK...	850
HTLV-II Pol	NRAKYLIEC	ENLEEDNATH	KAEWLNEN	VMNPSCKRW	QTHHSEPLP	900
HTLV-I Pol	TLEMKYFTEK	PDEEDNALS	IALWNLNEN	VLNCHKRW	QLHHSRLOP	814
Consensus	...NRAKYLIE...	ENLEEDNATH...	...KAEWLNEN...	...VMNPSCKRW...	...QTHHSEPLP...	900
HTLV-II Pol	TPASTPPKP	PPKRYMKKP	GLINQWKG	LSLOEAGAGA	ALLSIDGS-P	949
HTLV-I Pol	TPETRSLSNK	QTHMYMKKP	GLNSRQWKG	OELOEAGAGA	ALIPASASSA	864
Consensus	TP...ASTPPKP	...PPKRYMKKP...	GLINQWKG...	LSLOEAGAGA...	ALLSIDGS-P...	950
HTLV-II Pol	FWLPWFLLK	AAQPRDASE	LAHAATHO	HHG		982
HTLV-I Pol	QWLPWFLLK	AAQPRVGGP	ADPKKLO	HHG		896
Consensus	FWLPWFLLK	AAQPRDASE	LAHAATHO	HHG		983

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HTLV-I/II: HIV-1  
Pol Alignment

HTLV-II Pol	HRSRPYGYTP -DTRARAGKA PRHPDPR---	RCWANQH--	PVQTTPNPPT	43
HTLV-I Pol	GKKAACNLA- -----	--NTGAS--	RLPWA-----	21
HIV SF2 Pol	FFREDLAFFQ GKAREFSSEQ TRANSPTSRE	LRVWGRDNNS	PSEAGADRQG	50
Consensus	.....-.. --R..... .R...P.---	-E..WA.....	P...TP.....	50
HTLV-II Pol	HI-LALPKVP -RYPFLPLR HPQOMDH---	-----	-----HWKG	72
HTLV-I Pol	-----PKAP -R-----	-----	-----	26
HIV SF2 Pol	TVSFNLQIT LWQRPIVTIK IGGQLKEALL	DTGADDTVLE	EMNLPGRWKP	100
Consensus	...-..LEK.P -R..... ..Q....-	-----	-----WK.	100
HTLV-II Pol	RPTTMPGASI PPRR-----	-----	-----PQPPPI	102
HTLV-I Pol	-----	-----	-----	26
HIV SF2 Pol	KMIGGIGGFI KVRQYDQILI EICGHKAIGT	VLVGPTPVNI	IGRNLLTQLG	150
Consensus	.....G..I ..R.-----	-----	-----P.P..I .....	150
HTLV-II Pol	PRTPSPTSP- -SGEISFKKE -----RLQ--A	END-----	LV S--KAIE-AC	136
HTLV-I Pol	-----NQIPPFKKE -----RLQ--A	LOH-----	LV R--KAIE-AC	51
HIV SF2 Pol	CTLNFPISPI ETVEKIKKPG MDGPKVKQWP	ITEEKIKVLI	EICTEMEKEG	200
Consensus	.....P.SP- --..EV.FKKE -----RLQ--A	U..-----	LV .--KAIE-AC	200
HTLV-II Pol	HIEPYS--GE GNPVEVPKKK PNG-KWRFIH	ELRATNAIT	TLTSPSPGGE	183
HTLV-I Pol	HIEPYT--GE GNPVEVPKKK ANG-TWRFIH	ELRATNSLI	DLSSSSPGGE	98
HIV SF2 Pol	KISKVGPENP YNIPVEAIKK KSTKWKLV	DFRELKRIQ	DFWEVQLGIP	250
Consensus	HIEPY.--GE GNPVEVPKKK .NG-KWRFIH	ELRATN...I	DL.S.SPGE	250
HTLV-II Pol	DLISSEPTALP HLQTIIDLRDA FEQIPLPKQY	QRYFAFIMPO	PQNYGPGIRY	233
HTLV-I Pol	DLSSIPPTLA HLQTIIDLRDA FEQIPLPKQF	QRYFAFIMPO	QQNYGPGIRY	148
HIV SF2 Pol	HPAGLKKK-K SVTVLDVGDA MFSVPLKKEF	RKYIAFIMPS	INNETPGIRY	299
Consensus	DLISSEPT.L. HLQTIIDLRDA FEQIPLPKQF	QRYFAFIMPO	.QNYGPGIRY	300
HTLV-II Pol	AWIVLEPGGK NSPILFEQQLDAVENEMKRM	FETSTIVQYM	DEILLASPTN	283
HTLV-I Pol	AWKVLPGGK NSPILFEQQLAHILQPIRQA	FEOCTILOYM	DEILLASPSH	198
HIV SF2 Pol	QYNVLEPGWK GSPALFEQSSM IKKLEPFRKQ	NEDIVIMQYM	DELYVGSOLE	349
Consensus	AW.VLEPGGK NSPILFEQQLDAVENEMKRM	FETSTIVQYM	DEILLASPTN	350
HTLV-II Pol	EELQQLSOLT QALTTHTGLP ISQKTIQTP	GQIRFGQVI	SPNHITVEST	333
HTLV-I Pol	EDLLLLSEAT MASLISHGLP VGENKTIQTP	GTIKFGQII	SPNHITVEST	248
HIV SF2 Pol	IGQHRTKIEE IRQHLLRWGF TTPKKKQKE	PPFLWEGYEL	HPQKWIVQPI	399
Consensus	E.L..LS..T Q..L..HGLP .S..KTIQTP	G.I.FGQ.I	SPNHITVEST	400
HTLV-II Pol	PTIRIKSQWV LTELQVILGE IQWMSKGTP	LRKHLOSTYS	ALHGYRDPRA	383
HTLV-I Pol	PTVIRSRWV LTELQVILGE IQWMSKGTP	LRQPLHSLYC	ALQRTDPRD	298
HIV SF2 Pol	-MLEKDSWV VNLQKLVCK LNPASQIYAG	IK--VKKCK	LRGTALTE	446
Consensus	PTIRIKSQWV LTELQVILGE IQWMSKGTP	LR..L.SLY	AL.G..DPR.	450



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HTLV-II Pol	CHITTPQQLH	ATHAIGGATD	HNCRGRLNPA	LPLTGLISTE	TSGITTSVIFQ	433
HTLV-I Pol	CHIMNPQVQ	SLVQLRGALS	QNCRSRLVQT	LPLTGAIMET	LTGITTVVVFQ	348
HIV SF2 Pol	VIELTEEAEL	ETLAENREIILK	EPVHGYYVDP	SKLL-VAETQ	KQGQGWYTYQ	495
Consensus	.I.I.TP.Q..	.L...RQAL.	.NCRGRL...	LPLTG.I.L.	..GTT.V.FQ	500
HTLV-II Pol	PKQWFLAWL	HTPHPTSLC	PWGHLACTI	LTLPRMLOH	YGQLCQSFHH	483
HTLV-I Pol	SKQWPLVWL	HAPLPHTSQC	PWGQLLASAV	LLLPRMLOS	YGLLCQTIHH	398
HIV SF2 Pol	IYQE-FFKNL	KITGKYARMRG	AHTNDVKQLT	EAVKRTIDQS	IVIWGKIKPKF	544
Consensus	.KQ.WEL.WL	HDP.P.TS.C	PWG.LLA...	L.LPRMLOS	YG.LCQT.HH	550
HTLV-II Pol	NMSKQALC-D	FLRNSPHPSV	GILIHMGFR	HNTGSQPSGP	WKTLLHLPTL	532
HTLV-I Pol	NISTOTFN-Q	FIQTSDHPSV	HILLHSHRF	KNLGAQTGEL	WNITFLKTAAP	447
HIV SF2 Pol	KLPICKETWE	AWWTEYQOAT	WIPEWEFVNT	PHLVKLWYQL	EKDPIVGAET	594
Consensus	N.S.Q....	F..TS.HPSV	.ILL.HH..RF	.NKG.Q...L	WKT.L.L.A..	600
HTLV-II Pol	LQEPRLLRPI	FTLSPVVLIT	APCLFSDGSP	QKAYVVLWDQ	TILQQDITPL	582
HTLV-I Pol	LAPVKALMPV	FTLSPVIINT	APCLFSDGST	SRAAYILWK	QILSQRSFPL	497
HIV SF2 Pol	FYVDGAANRE	TKLGKAGYVT	DRGRQKVSL	TDITNQKTSL	QAIHLALQDS	644
Consensus	L....AL.P.	FTLSPV...IT	APCLFSDGS.	...AAY.LWD.	QIL.Q...PL	650
HTLV-II Pol	PSHETHSACK	GELLALICGL	RAAKPWPSLN	IFLDSKYLK	YLHSLAIGAF	632
HTLV-I Pol	PPPH-KSAQR	AELLGLLHGL	SSARSWRCLN	IFLDSKYLH	YLRTIALGTF	546
HIV SF2 Pol	GLEVNIVIDS	QYALGIIQAQ	PKSESELVS	QIIEQLIKKE	KVYLAWWPAH	694
Consensus	P.....SAQ.	.ELLGLI.GL	..A..W..LN	IFLDSKYL..	YL..LA.GAF	700
HTLV-II Pol	IGTSAHQTLQ	AALPPLLQCK	TIYHHRSH	TNLPPPISTF	NEYTDSHILA	682
HTLV-I Pol	QGRSSQAPFO	ALLPRLLSRK	VVYLHHRSH	TNLPPPI SRL	NALTDALLIT	596
HIV SF2 Pol	KGIGGNEQVD	KLVSAGI-RK	VLFLDGL---	DKAQEEHEKY	HSNWRAM---A	738
Consensus	.G.S.....Q	ALLP.LL.RK	V.YLHHRSH	TNLPPPI S..	N..TDAL..A	750
HTLV-II Pol	PLVHQLQGL	HGLTHCNQRA	LVSFGATPRE	AKSLVQICHT	QYTINSQHHM	732
HTLV-I Pol	PVLQISEAEL	HSFTHCGQTA	LTLQGATTTE	ASNILRECHA	GRGGNPQHOM	646
HIV SF2 Pol	SDFNQLFE---	-----VV-----	-----	AKETVAGCDK	QQ--LKGEAM	765
Consensus	P...L.L	H..THC.Q.A	LV..GAT..E	AK.IV.SCH.	QQ..N.QH.M	800
HTLV-II Pol	PRGYRRGLL	ENHINCGEM	EFKYKRYKYC	LEVWVDTFSG	AMSVSCKKKE	782
HTLV-I Pol	PRGHRRGLL	ENHINCGEII	EFKYKNTLYR	LEVWVDTFSG	AMSATQKRKE	696
HIV SF2 Pol	-HQQDCS--	EG-IVQLDCT	ILEGKIILVA	VHV-ASGY--	-EEAEVIPAE	807
Consensus	PRG..RRGLL	ENHINCGE..	..E.KYK..LY.	LEVWVDTFSG	AMSA..K.KK	850
HTLV-II Pol	ISCEHISAVL	QAISLLGKPL	HININENGP	ISQEFQEFCT	SYRIKSTHII	832
HTLV-I Pol	ISSEISSLK	QAIAHLGKPS	YININENGP	ISQDFLNMCT	SLAIRATTHV	746
HIV SF2 Pol	IGQDAYFID	KLGRWVPVKT	-HINENGSNF	TSITTVKAACW	WAGIKQEFGL	856
Consensus	IS.EHIS..L	QAI..LGKP.	..ININENGP	.SQ.F...CT	S...IKH..THI	900



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HTLV-II Pol	PYNHISSELVVERINGVIKNL	LNKYLDCPN	PLDNAIHKA	LWTLNQLNVM	882
HTLV-I Pol	PYNHISSELVVERINGVIKNL	LYKYFTKPD	PMDNALSIA	LWTINHLNVL	796
HIV SF2 Pol	PYNHISSELVVERINGVIKNI	IGQVRDQAEH	KTAVQMAVF	IHNFKRKGGI	906
Consensus	PYNHISSELVVERINGVIK.L	L.KY..D.P.	P.DNA...A	LWT.N.LNV.	950

HTLV-II Pol	NPSGKTRWQI	HHSPPLPIPI	EASTPPKPPP	KWFYKLPGL	TNQRWKGLQ	932
HTLV-I Pol	TNCHKTRWQL	HHSPRLQPIP	STRSLSNKQT	HWYYFKLPGL	NSRQWKGPQE	846
HIV SF2 Pol	GGYSAGERIV	DIIATDIQTK	ELQKQITKIQ	NFRVY-YRDS	REPLWKGPAAK	955
Consensus	....KTRWQ.	HHSP.L.PIP	E.....K..	.W.YYKLPGL	....WKGP..	1000

HTLV-II Pol	STQEAAGAAL	LSIEGS-PRW	TEWRFLKAA	CPRPDASELA	EHAATDHH	981
HTLV-I Pol	ATQEAAGAAL	IPVSASSAQW	TEWRLLKRAA	CPRPVGGP-A	DPKEKDLOHH	895
HIV SF2 Pol	LLWKGECAVV	IQDNSD-IKV	MPRR--KAKI	IRDYGKQ MAG	DDCVASRDE	1002
Consensus	..QEAAGAAL	I...S...W	TEWR.LK.AA	CPRP.....A	D.....D.QHH	1050

HTLV-II Pol	G					982
HTLV-I Pol	G					896
HIV SF2 Pol	D					1003
Consensus	G					1051

# Untitled-13 Formatted Alignment

HTLV-I/II  
GAG ALIGNMENT

HTLV-II Gag	MGQIHGLSPT PTPKAPRGES THHWLNELQA AYRIEPPSD FDRQOIRRET	50
HTLV-I gag	MGQIFSRAS PTPRHPRGIA THHWLNELQA AYRIEPPSS YDRFOIKRET	50
Consensus	MGQH...S... PTP...PRGI... THHWLNELQA AYRI...PS... DR...IR...ET	50
HTLV-II Gag	KIATKTHIWL NPTIYSLIAS LIPKGYPCRV VETILNITAKN QVSPSAPAAP	100
HTLV-I gag	KIALETTPARI QPNIYSLIAS LIPKGYPCRV NETHLITITQT Q-----AQ	93
Consensus	K...AT...TH... P...I...Y...S...L...I...A...S... L...I...P...K...G...Y...P...C...R...V... V...E...T...I...L...N...I...T...A...K...N... Q...V...S...P...S...A...P...A...P...	100
HTLV-II Gag	VETPICPTTT PEPPEPESP -----FAHV PPPEVETPIT QCFETLTFEC	143
HTLV-I gag	IESR----- PEPPEPESP HDPPDSIPQI PPPEVETPAP QVLEWMTFEC	137
Consensus	V...E...T...P...I...C...P...T...T...T... P...E...P...P...E...P...E...P...S...P...T...P...P...P...D...S...I...P...Q...I... P...P...P...E...V...E...T...P...I...T... Q...C...F...E...T...L...T...F...E...C...	150
HTLV-II Gag	APSAHREWOM KDLOAIKQEV SSSALGSPQF MOTI RLAVQQ FQPTAKDLOQ	193
HTLV-I gag	APNHREWOM KDLOAIKQEV SQALGSPQF MOTIRLAVQQ FQPTAKDLOQ	187
Consensus	A...P...S...A...H...R...E...W...O...M... K...D...L...O...A...I...K...Q...E...V... S...S...S...A...L...G...S...P...Q...F... M...O...T...I... R...L...A...V...Q...Q... F...Q...P...T...A...K...D...L...O...Q...	200
HTLV-II Gag	LLOYLCSLV VSLHOOQNT LITSEAEIRGM IGVNEVAGPL RVOANNPAQQ	243
HTLV-I gag	LLOYLCSLV VSLHOOQLS LITSEAEIRGI IGVNEVAGPL RVOANNPAQQ	237
Consensus	L...L...O...Y...L...C...S...S...L...V... V...S...L...H...O...O...Q...N...T... L...I...T...S...E...A...E...I...R...G...M... I...G...V...N...E...V...A...G...P...L... R...V...O...A...N...N...P...A...Q...Q...	250
HTLV-II Gag	GLRREYQELW LAEASILPGN TRDPSWASIL QGLEEPPYCAF VERLENVAHEN	293
HTLV-I gag	GLRREYQELW LAEFAALPGS AKDPSWASIL QGLEEPPYCAF VERLENVAHEN	287
Consensus	G...L...R...R...E...Y...Q...E...L...W... L...A...E...A...S...I...L...P...G...N... T...R...D...P...S...W...A...S...I...L... Q...G...L...E...E...P...P...Y...C...A...F... V...E...R...L...E...N...V...A...H...E...N...	300
HTLV-II Gag	GLPEGTPEKP IERSLAYSNA NKECOKILOA RCHTNSPLGE MLRIQCAWIE	343
HTLV-I gag	GLPEGTPEKP IERSLAYSNA NKECOKILOA RCHTNSPLGD MLRACQIWIIE	337
Consensus	G...L...P...E...G...T...P...E...K...P... I...E...R...S...L...A...Y...S...N...A... N...K...E...C...O...K...I...L...O...A... R...C...H...T...N...S...P...L...G...E... M...L...R...I...Q...C...A...W...I...E...	350
HTLV-II Gag	KDKKLVAVVQ ERPEPTDPC FRCKVGHWS RDCTOPRPPP GPCPLCODES	393
HTLV-I gag	KDKKLVAVVQ EKPPENQPC FRCKVGHWS RDCTOPRPPP GPCPLCODET	387
Consensus	K...D...K...K...L...V...A...V...V...Q... E...R...P...E...P...T...D...P...C... F...R...C...K...V...G...H...W...S... R...D...C...T...O...P...R...P...P...P... G...P...C...P...L...C...O...D...E...S...	400
HTLV-II Gag	HWKRDCEPILK -----POHEG SHHMDIST STGTTEKNSL RGIH	433
HTLV-I gag	HWKRDCEPILK ETIPEPEEE SHHMDIST-- SDIPHEKFI GOEV	429
Consensus	H...W...K...R...D...C...E...P...I...L...K... P...O...H...E...G... S...H...H...M...D...I...S...T... S...T...G...T...T...E...K...N...S...L... R...G...I...H...	444

# Untitled-13 Formatted Alignment

HTLV-I/II: HIV-I  
GAG ALIGNMENT

HTLV-II Gag	MSQIHG-LSP	TPIPKAPRGL	STHHWLNFLQ	AAYRLQPRPS	DFLEQOLRRF	49
HTLV-I gag	MSQIFS-RSA	SPIPRPPRGL	AAHHWLNFLQ	AAYRLEPGPS	SYDFHQLKKF	49
Hiv SF2 Gag	MGARASVLSG	GELDKWEKIR	LRPGGKKKYQ	LKHIVWASRE	LERTAINPGL	50
Consensus	MSQI.S-LS	.PIPK.PRGL	..HHWLNFLQ	AAYRL.P.PS	..DEQL..F	50
HTLV-II Gag	TKLALKTPIW	LNPIFYSLA	SLIPKGYPR	VVEIINILVK	NOVSPSAPAA	99
HTLV-I gag	TKIALETGAR	ICPINYSLA	SLLPKGYPR	VNEILHILIQ	TQ-----A	92
Hiv SF2 Gag	LETSEGCRQI	LGQLQPSLKP	GSEEIRSLYN	TVATLYCVHQ	KIEVKDTKEA	100
Consensus	TK.AL.TP..	L.PIYSLA	SL.PKGYPR	VVEIL.IL.Q	.Q.....A	100
HTLV-II Gag	FVPTPICPTT	TPPPPPPPSP	-----EAH	VHPYVEPTT	TQCFPILHPP	142
HTLV-I gag	QIPSR-----	-PAPPPPPSSP	THDPPDSDPQ	IHPYVEPTA	PQVLPVMHPH	136
Hiv SF2 Gag	LDKIEEEQNK	SKKKAQQTAA	DTGNSSQVSO	NYETIVQNLQ	QMVHQPISEK	150
Consensus	..P.....	.P.PPPP.SP	.....Q	.HPYVEPT.	.QV.P..HE	150
HTLV-II Gag	GAPSAHRPWQ	MDL-QATKQ	EVSSSALG-S	EQFMQILRLA	MQQFDPTAKD	190
HTLV-I gag	GAPNHRPWQ	MDL-QATKQ	EVSQAALG-S	EQFMQILRLA	MQQFDPTAKD	184
Hiv SF2 Gag	TLNAWVKVVE	EKAFSPENIP	MFSALAECAI	PDQNLIMLNI	VGGHQAAMQM	200
Consensus	GAP..HRPWQ	MDL-QATKQ	EVS..A.G-S	EQFMQILRLA	MQQFDPTAKD	200
HTLV-II Gag	LDQLLYLCS	SL--VVSLEH	QQLN-TLITE	AETRGMIGYN	PMAGPLRMQA	237
HTLV-I gag	LDQLLYLCS	SL--VASLEH	QQLD-SLISE	AETRGIIGYN	PLAGPLRVQA	231
Hiv SF2 Gag	DKETINEEAA	EWDRLLHPVHA	GPIAPGQMRP	PRGSDIAGTT	STLQEQIGWM	250
Consensus	LDQLLYLCS	SL--V.SLEH	QQL..-LI.E	AETRGIIGYN	P.AGPLR.QA	250
HTLV-II Gag	NMPAQOGLRR	EYQNLWLAFF	STLPGNTRDP	SWAATLOGLE	EPYCAFVERL	287
HTLV-I gag	NMPQOQGLRR	EYQQLWLAFF	ALPGSAKDP	SWASITLOGLE	EPYHAFVERL	281
Hiv SF2 Gag	TNNPPIPVGE	IKRWIILGL	NKIVRMYSPT	SILLIRQGP	EPFRDYVIRF	300
Consensus	NMP.QOGLRR	EYQ.LWLAFF	.LPG...DP	SWA..ILOGLE	EPY..AFVERL	300
HTLV-II Gag	NVIEDNGLPE	GTHKIPILRS	TAYSNANKEC	OKILQARCHI	NSHLEGEMIRA	337
HTLV-I gag	NIEDNGLPE	GTHKIPILRS	TAYSNANKEC	OKILQARCHI	NSHLEGEMIRA	331
Hiv SF2 Gag	YKIERREQAS	QDVKNWMTED	ELVQANPFC	KTILKALCPA	ATILEEMMTA	349
Consensus	N..IDNGLPE	GTHKIPILRS	TAYSNANKEC	OKILQARCHI	NSHLEGEMIRA	350
HTLV-II Gag	CGAW-TIEKDK	IKRM-----	-----VVQP	---RRPPPTQ	FEIRGCKVCH	371
HTLV-I gag	CGIW-TIEKDK	IKRM-----	-----VVQP	---KKPPPNQ	FEIRGCKVCH	365
Hiv SF2 Gag	CGVGGEQGHK	SRVAEAMSQ	VNSVTVMQK	GNFKNQKTV	KGRNCKKECH	399
Consensus	CG.W-TIEKDK	IKRM-----	-----VVQP	---K.PPPTQ	FEIRGCKVCH	400
HTLV-II Gag	WSREITQEP	PPG-PC----	-PE--QDP-	-----SHA--	KRDCI-----Q	401
HTLV-I gag	WSREITQEP	PPG-PC----	-PE--QDP-	-----THA--	KRDCI-----R	395
Hiv SF2 Gag	IKNCRAPRK	KGCWKCGREG	HOMKICITRQ	ANFLGKIDPS	HKGREGNFIQ	449
Consensus	WSREITQEP	PPG-PC----	-PE--QDP-	-----HA--	KRDCI-----Q	450

# Untitled-13 Formatted Alignment

HTLV-II Gag	LK <b>E</b> --- <b>E</b> QE <b>E</b> ---GE---PLLL <b>E</b> ST SG---TTEEK <b>E</b> SLRGE <b>E</b> ---	433
HTLV-I gag	LKETIPEPE <b>E</b> --- <b>E</b> --- <b>E</b> ---ALL <b>E</b> AD---IPHPK <b>E</b> FIGGE <b>E</b> ---	429
Hiv SF2 Gag	NRPEPTAPPA <b>E</b> SFGFG <b>E</b> ETT TPQ <b>E</b> KE <b>E</b> ID KGLYPLTSLR <b>E</b> SLFGNDPSSQ	499
Consensus	L <b>E</b> .... <b>E</b> .. <b>E</b> ---GE---PLLL <b>E</b> ... .G---.T..K N..G <b>E</b> ....	500